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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/939,483

DATE: 09/13/2001
 TIME: 11:24:55

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3 <110> APPLICANT: Duprat, Fabrice
 4 Lesage, Florian
 5 Fink, Michel
 6 Lazdunski, Michel
 8 <120> TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
 9 AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
 11 <130> FILE REFERENCE: 1201-CIP-DIV-2-00
 W--> 13 <140> CURRENT APPLICATION NUMBER: US/09/939,483 OK
 13 <141> CURRENT FILING DATE: 2001-08-24
 15 <150> PRIOR APPLICATION NUMBER: 09/144,914
 16 <151> PRIOR FILING DATE: 1998-09-01
 18 <150> PRIOR APPLICATION NUMBER: 08/749,816
 19 <151> PRIOR FILING DATE: 1996-11-15
 21 <150> PRIOR APPLICATION NUMBER: 60/095,234
 22 <151> PRIOR FILING DATE: 1998-08-04
 24 <150> PRIOR APPLICATION NUMBER: FR 96/01565
 25 <151> PRIOR FILING DATE: 1996-02-08
 27 <160> NUMBER OF SEQ ID NOS: 24
 29 <170> SOFTWARE: PatentIn Ver. 2.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1894
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (183)..(1190)
 40 <220> FEATURE:
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 43 <400> SEQUENCE: 1
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 48 cgcgctccgg ccggtctgcg gcgttggcct tggctttggc tttggcgggc gcggtggaga 180
 50 ag atg ctg cag tcc ctg gcc ggc agc tcg tgc gtg cgc ctg gtg gag 227
 51 Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu
 52 1 5 10 15
 54 cgg cac cgc tcg gcc tgg tgc ttc ggc ttc ctg gtg ctg ggc tac ttg 275
 55 Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu
 56 20 25 30
 58 ctc tac ctg gtc ttc ggc gca gtg gtc ttc tcc tcg gtg gag ctg ccc 323
 59 Leu Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro
 60 35 40 45
 62 tat gag gac ctg ctg cgc cag gag ctg cgc aag ctg aag cga cgc ttc 371
 63 Tyr Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe
 64 50 55 60
 66 ttg gag gag cac gag tgc ctg tct gag cag cag ctg gag cag ttc ctg 419
 65 70 75
 65 Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu

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70 ggc cgg gtg ctg gag gcc agc aac tac ggc gtg tcg gtg ctc agc aac 467
71 Gly Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn
72 80 85 90 95
74 gcc tcg ggc aac tgg aac tgg gac ttc acc tcc gcg ctc ttc ttc gcc 515
75 Ala Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala
76 100 105 110
78 agc acc gtg ctc tcc acc aca ggt tat ggc cac acc gtg ccc ttg tca 563
79 Ser Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser
80 115 120 125
82 gat gga ggt aag gcc ttc tgc atc atc tac tcc gtc att ggc att ccc 611
83 Asp Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro
84 130 135 140
86 ttc acc ctc ctg ttc ctg acg gct gtg gtc cag cgc atc acc gtg cac 659
87 Phe Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His
88 145 150 155
90 gtc acc cgc agg ccg gtc ctc tac ttc cac atc cgc tgg ggc ttc tcc 707
91 Val Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser
92 160 165 170 175
94 aag cag gtg gtg gcc atc gtc cat gcc gtg ctc ctt ggg ttt gtc act 755
95 Lys Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr
96 180 185 190
98 gtg tcc tgc ttc ttc ttc atc ccg gcc gct gtc ttc tca gtc ctg gag 803
99 Val Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu
100 195 200 205
102 gat gac tgg aac ttc ctg gaa tcc ttt tat ttt tgt ttt att tcc ctg 851
103 Asp Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu
104 210 215 220
106 agc acc att ggc ctg ggg gat tat gtg cct ggg gaa ggc tac aat caa 899
107 Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln
108 225 230 235
110 aaa ttc aga gag ctc tat aag att ggg atc acg tgt tac ctg cta ctt 947
111 Lys Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu
112 240 245 250 255
114 ggc ctt att gcc atg ttg gta gtt ctg gaa acc ttc tgt gaa ctc cat 995
115 Gly Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His
116 260 265 270
118 gag ctg aaa aaa ttc aga aaa atg ttc tat gtg aag aag gac aag gac 1043
119 Glu Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp
120 275 280 285
122 gag gat cag gtg cac atc ata gag cat gac caa ctg tcc ttc tcc tcg 1091
123 Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser
124 290 295 300
126 atc aca gac cag gca gct ggc atg aaa gag gac cag aag caa aat gag 1139
127 Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu
128 305 310 315
130 cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac 1187
131 Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn
132 320 325 330 335
134 cat tgagcgtagg atttggtgca ttatgctaga gcaccagggt cagggtgcaa 1240

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135 His
137 ggaagaggct taagtatggt cattttttatc agaatgcaaa agcgaaaatt atgtcacttt 1300
139 aagaaatagc tactgtttgc aatgtcttat taaaaaacia caaaaaaaga cacatggaac 1360
141 aaagaagctg tgaccccagc aggatgtcta atatgtgagg aaatgagatg tccacctaaa 1420
143 attcatatgt gacaaaatta tctcgacctt acataggagg agaatacttg aagcagtatg 1480
145 ctgctgtggt tagaagcaga ttttataactt ttaactggaa actttgggggt ttgcatttag 1540
147 atcatttagc tgatggctaa atagcaaaat ttatatattag aagcaaaaaa aaaaagcata 1600
149 gagatgtggt ttataaatag gtttatgtgt actgggtttgc atgtaccac ccaaatgat 1660
151 tatttttggga gaatctaagt caaactcact atttataatg cataggtaac cattaactat 1720
153 gtacatataa agtataaata tgtttatatt ctgtacatat ggtttagggtc accagatcct 1780
155 agtgtagtgc tgaaactaag actatagata ttttgtttct tttgatttct ctttatacta 1840
157 aagaatccag agttgctaca ataaaataag gggaataata aaaaaaaaaa aaaa 1894
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161 <211> LENGTH: 336
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <223> OTHER INFORMATION: TWIK-1
168 <400> SEQUENCE: 2
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172 His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
173 20 25 30
175 Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
176 35 40 45
178 Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
179 50 55 60
181 Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
182 65 70 75 80
184 Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
185 85 90 95
187 Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
188 100 105 110
190 Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
191 115 120 125
193 Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
194 130 135 140
196 Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
197 145 150 155 160
199 Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
200 165 170 175
202 Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
203 180 185 190
205 Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp
206 195 200 205
208 Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
209 210 215 220
211 Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
212 225 230 235 240

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214 Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly
215                245                250                255
217 Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
218                260                265                270
220 Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
221                275                280                285
223 Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile
224                290                295                300
226 Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
227 305                310                315                320
229 Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn His
230                325                330                335

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233 <210> SEQ ID NO: 3

234 <211> LENGTH: 2514

235 <212> TYPE: DNA

236 <213> ORGANISM: Homo sapiens

238 <220> FEATURE:

239 <221> NAME/KEY: CDS

240 <222> LOCATION: (126)..(1307)

242 <220> FEATURE:

243 <223> OTHER INFORMATION: TASK

245 <400> SEQUENCE: 3

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250 ggacg atg aag cgg cag aac gtg cgc acg ctg gcg ctc atc gtg tgc acc 170
251      Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr
252          1          5          10          15
254 ttc acc tac ctg ctg gtg ggc gcc gcg gtc ttc gac gcg ctg gag tcg 218
255 Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser
256          20          25          30
258 gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266
259 Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu
260          35          40          45
262 ctg cgg gcg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314
263 Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu
264          50          55          60
266 cgc gtc gtg ctg cgc ctc aag ccg cac aag gcc ggc gtg cag tgg cgc 362
267 Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg
268          65          70          75
270 ttc gcc ggc tcc ttc tac ttc gcc atc acc gtc atc acc acc atc ggc 410
271 Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly
272 80          85          90          95
274 tac ggg cac gcg gca ccc agc acg gat ggc ggc aag gtg ttc tgc atg 458
275 Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met
276          100          105          110
278 ttc tac gcg ctg ctg ggc atc ccg ctc acg ctc gtc atg ttc cag agc 506
279 Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser
280          115          120          125
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283	Leu	Gly	Glu	Arg	Ile	Asn	Thr	Leu	Val	Arg	Tyr	Leu	Leu	His	Arg	Ala		
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286	aag	aag	ggg	ctg	ggc	atg	cgg	cgc	gcc	gac	gtg	tcc	atg	gcc	aac	atg	602	
287	Lys	Lys	Gly	Leu	Gly	Met	Arg	Arg	Ala	Asp	Val	Ser	Met	Ala	Asn	Met		
288		145					150					155						
290	gtg	ctc	atc	ggc	ttc	ttc	tcg	tgc	atc	agc	acg	ctg	tgc	atc	ggc	gcc	650	
291	Val	Leu	Ile	Gly	Phe	Phe	Ser	Cys	Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala		
292	160						165				170					175		
294	gcc	gcc	ttc	tcc	cac	tac	gag	cac	tgg	acc	ttc	ttc	cag	gcc	tac	tac	698	
295	Ala	Ala	Phe	Ser	His	Tyr	Glu	His	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr		
296					180					185					190			
298	tac	tgc	ttc	atc	acc	ctc	acc	acc	atc	ggc	ttc	ggc	gac	tac	gtg	gcg	746	
299	Tyr	Cys	Phe	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala		
300			195						200					205				
302	ctg	cag	aag	gac	cag	gcc	ctg	cag	acg	cag	ccg	cag	tac	gtg	gcc	ttc	794	
303	Leu	Gln	Lys	Asp	Gln	Ala	Leu	Gln	Thr	Gln	Pro	Gln	Tyr	Val	Ala	Phe		
304		210					215						220					
306	agc	ttc	gtc	tac	atc	ctt	acg	ggc	ctc	acg	gtc	atc	ggc	gcc	ttc	ctc	842	
307	Ser	Phe	Val	Tyr	Ile	Leu	Thr	Gly	Leu	Thr	Val	Ile	Gly	Ala	Phe	Leu		
308		225					230					235						
310	aac	ctc	gtg	gtg	ctg	cgc	ttc	atg	acc	atg	aac	gcc	gag	gac	gag	aag	890	
311	Asn	Leu	Val	Val	Leu	Arg	Phe	Met	Thr	Met	Asn	Ala	Glu	Asp	Glu	Lys		
312	240					245				250					255			
314	cgc	gac	gcc	gag	cac	cgc	gcg	ctg	ctc	acg	cgc	aac	ggg	cag	gcg	ggc	938	
315	Arg	Asp	Ala	Glu	His	Arg	Ala	Leu	Leu	Thr	Arg	Asn	Gly	Gln	Ala	Gly		
316					260					265					270			
318	ggc	ggc	gga	ggg	ggt	ggc	agc	gcg	cac	act	acg	gac	acc	gcc	tca	tcc	986	
319	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Ala	His	Thr	Thr	Asp	Thr	Ala	Ser	Ser		
320			275						280					285				
322	acg	gcg	gca	gcg	ggc	ggc	ggc	ggc	ttc	cgc	aac	gtc	tac	gcg	gag	gtg	1034	
323	Thr	Ala	Ala	Ala	Gly	Gly	Gly	Gly	Phe	Arg	Asn	Val	Tyr	Ala	Glu	Val		
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326	ctg	cac	ttc	cag	tcc	atg	tgc	tcg	tgc	ctg	tgg	tac	aag	agc	cgc	gag	1082	
327	Leu	His	Phe	Gln	Ser	Met	Cys	Ser	Cys	Leu	Trp	Tyr	Lys	Ser	Arg	Glu		
328		305					310					315						
330	aag	ctg	cag	tac	tcc	atc	ccc	atg	atc	atc	ccg	cgg	gac	ctc	tcc	acg	1130	
331	Lys	Leu	Gln	Tyr	Ser	Ile	Pro	Met	Ile	Ile	Pro	Arg	Asp	Leu	Ser	Thr		
332	320					325					330					335		
334	tcc	gac	acg	tgc	gtg	gag	cag	agc	cac	tcg	tcg	ccg	gga	ggg	ggc	ggc	1178	
335	Ser	Asp	Thr	Cys	Val	Glu	Gln	Ser	His	Ser	Ser	Pro	Gly	Gly	Gly	Gly		
336					340					345					350			
338	cgc	tac	agc	gac	acg	ccc	tcg	cga	cgc	tgc	ctg	tgc	agc	ggg	gcg	cca	1226	
339	Arg	Tyr	Ser	Asp	Thr	Pro	Ser	Arg	Arg	Cys	Leu	Cys	Ser	Gly	Ala	Pro		
340			355						360					365				
342	cgc	tcc	gcc	atc	agc	tcg	gtg	tcc	acg	ggt	ctg	cac	agc	ctg	tcc	acc	1274	
343	Arg	Ser	Ala	Ile	Ser	Ser	Val	Ser	Thr	Gly	Leu	His	Ser	Leu	Ser	Thr		
344		370					375						380					
346	ttc	cgc	ggc	ctc	atg	aag	cgc	agg	agc	tcc	gtg	tgactgcccc	gagggacctg	1327				
347	Phe	Arg	Gly	Leu	Met	Lys	Arg	Arg	Ser	Ser	Val							

VERIFICATION SUMMARY

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TIME: 11:24:56

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